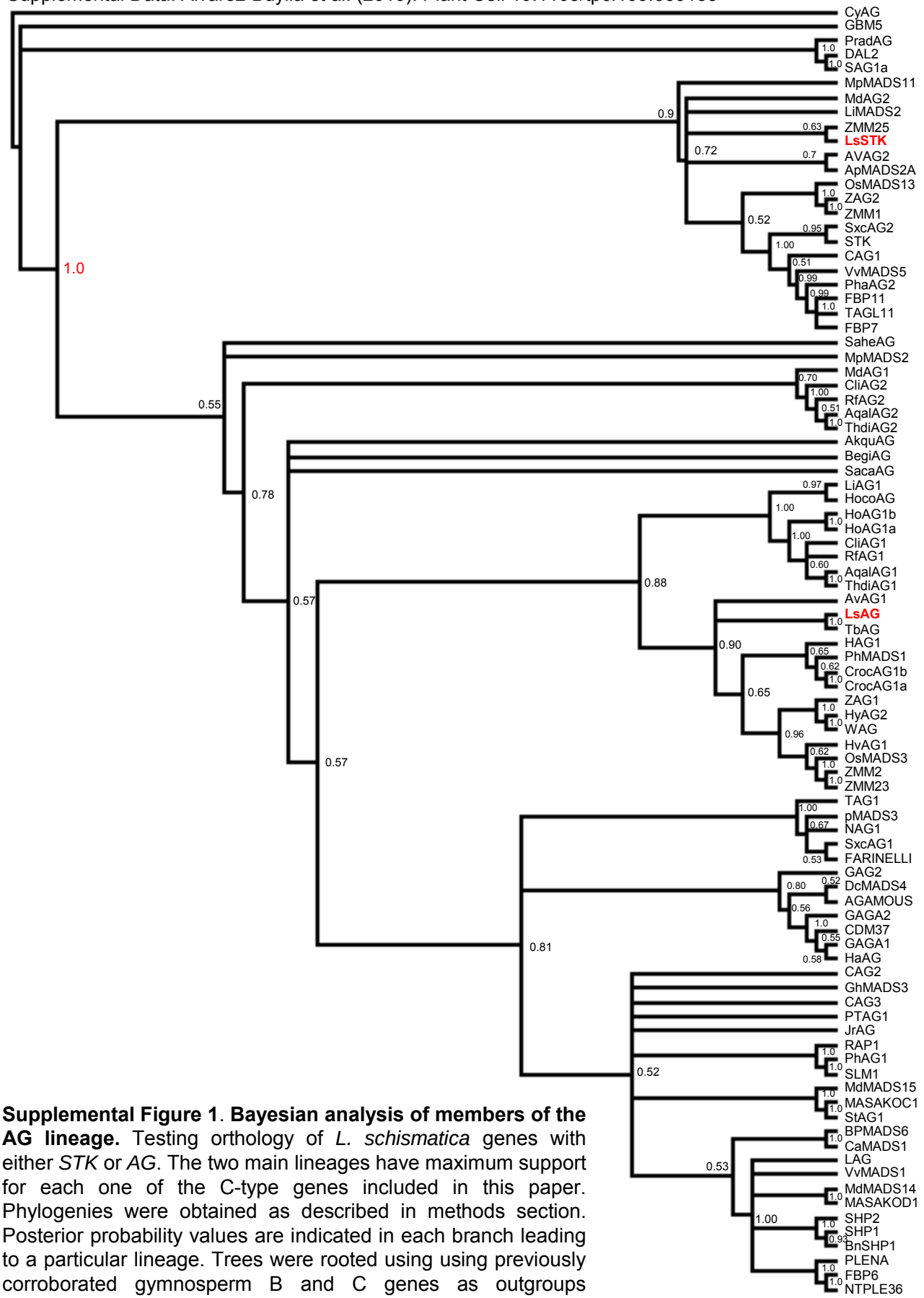
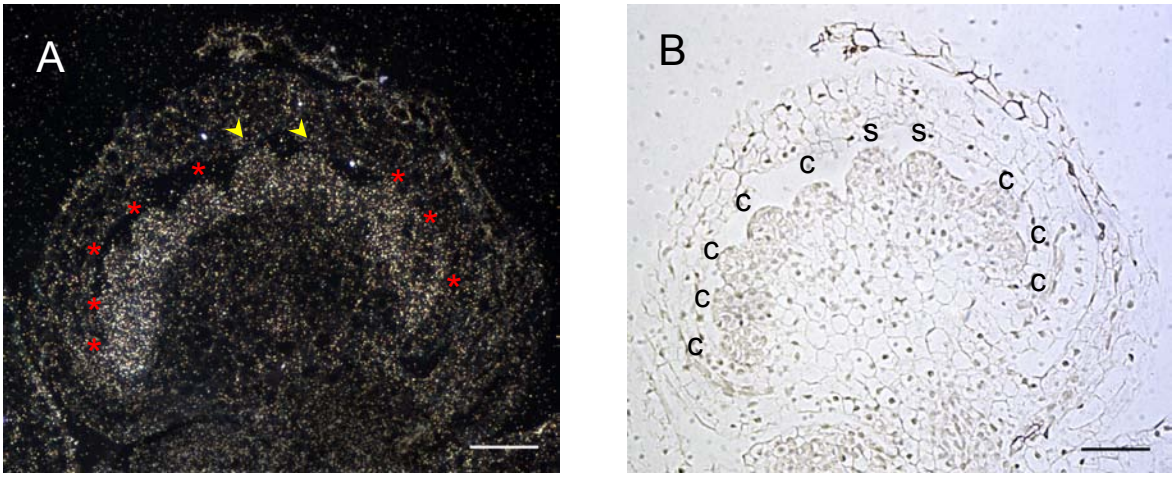
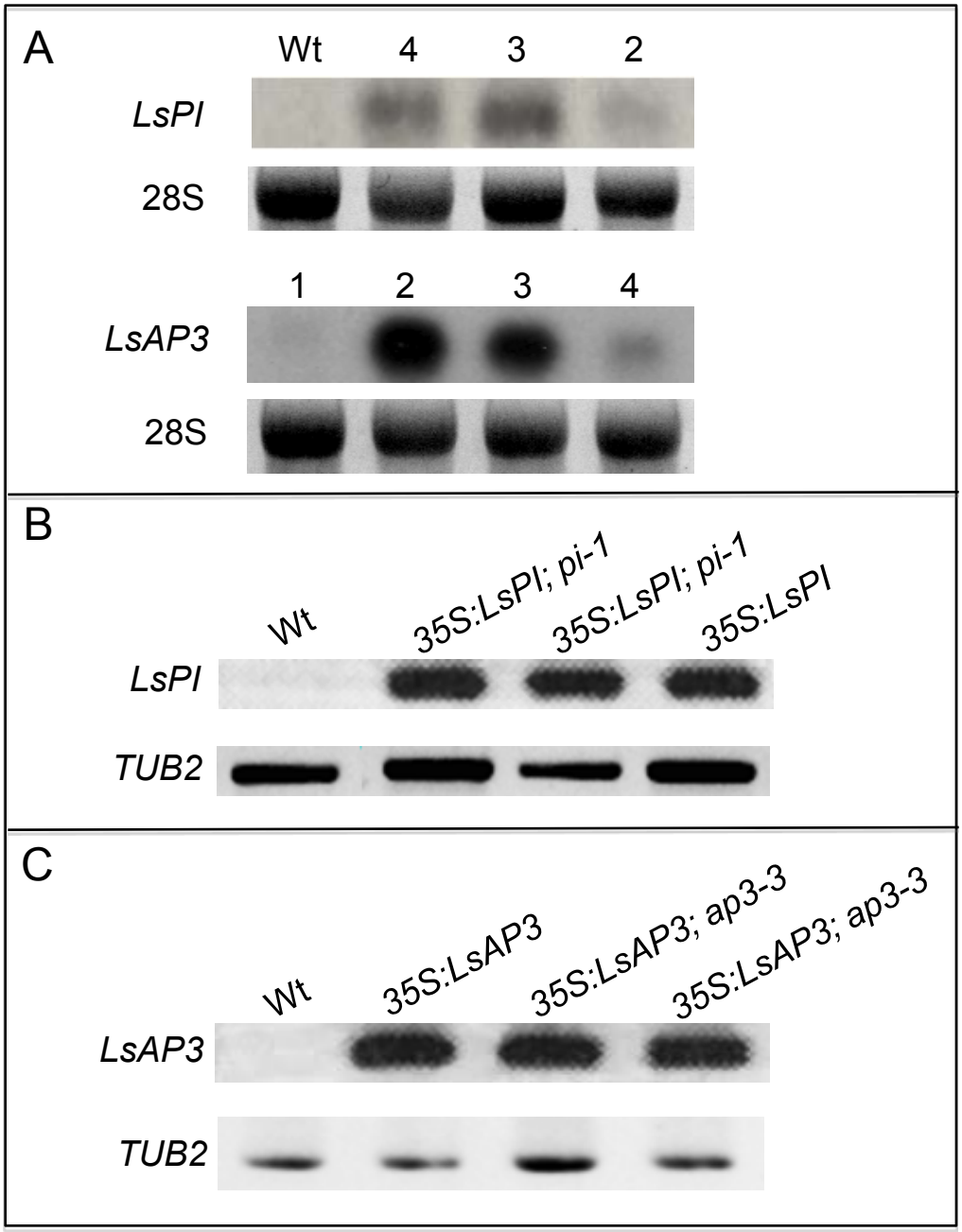


Supplemental Figure 1. **Bayesian analysis of members of the AG lineage.** Testing orthology of *L. schismatica* genes with either *STK* or *AG*. The two main lineages have maximum support for each one of the C-type genes included in this paper. Phylogenies were obtained as described in methods section. Posterior probability values are indicated in each branch leading to a particular lineage. Trees were rooted using using previously corroborated gymnosperm B and C genes as outgroups (Sundstrom, et al., 1999).



Supplemental Figure 2. Ls-*PI in situ* localization.
(A) *In situ* hybridization of *LsPi*-antisense probe showing expression in carpels (red asteriks) and stamens (yellow arrowheads) in the *L. schismatica* bud. (B) Bright field of (A) for reference. Carpels (c) and stamens (s). Scale bar represent 100 µm.



Supplemental Figure 3. **Expression of Ls-*AP3* and Ls-*PI* in overexpression and complementation lines.** (A*)* Ls-*AP3 and* Ls-*PI* mRNA accumulation in *35S:AtAP3* (lines ABA13 1-4) and *35S:AtPI* (lines ABA30 2-4) detected by RNA gel blot hybridization. (B) RT-PCR of Ls-*PI* and (C) Ls-*AP3* in F2 segregating lines in their respective mutant backgrounds. Two examples of complementation lines, one overexpressor line in wild type background and a wild-type plant, from their respective crosses shown in Figure 4 (see methods). Expression patterns in the individuals of the segregating F2 population (mutants not included here) correlate with phenotypes, and both segregate with expected ratios (see Supplemental Table 1).

Supplemental Table 1. Primers sequences used for 5´and 3´RACE.

3’ RACE primers:

All primer sequences were designed based on a consensus sequence of the MADS-box and were used in conjunction with the UAP and AUAP primers provided in the Invitrogen® 3’ and 5’ RACE kits.

Gene-specific primers:

For the MADS-box

DEFAPzero: 5’ TGA CCT ACT CCA AGC GCC 3’

DEFAP1: 5’ AGA T(C/T)A AG(C/A) GGA T(C/A)G A(G/A)A AC 3’

For *AP3* and *PI*:

DEFAP2: 5’ TGA CCT ACT CCA AGC GCC 3’

PIGL1: 5’ GAC ATC AAG AGG ATC GAC AAC 3’

For *AG*/*STK*:

01LAG: 5’ CCCAACAGCAGTTCAATATC 3’

03LAG: 5’ GAGGCAGCAGATAACAAACCTGCTG 3’

5’ RACE

For *AP3* and *PI*:

PIGL4: 5’ TGA CAG AGA TAG ACA TCC 3'

PIGL5: 5’ CTT GTC TAT ACT GGT CAG AG 3’

PIGL13: 5’ TTT GGC TGG AAT GGC TGG AC 3’

DEFAP6: 5’ ATC ACA CAC AGC AAC AGT AGG 3’

DEFAP10: 5’ TAG GCA AGA CGA AGG TCA TGG 3’

DEFAP11: 5’ ATG AGG TGG AGA TTG GGC 3’

For *AG*/*STK*:

4aBPG5: 5’ TGC ATA GTT AGC TCC CTC TAC 3’

4Abpg4: 5’ AGT CTA TCT GCA TAG TTA GC 3’

LsAG1-GSP1: 5’ ACA TGT ATT TGA GGA ACA AGA T 3’

NestedLsAG1: 5’ CCA CCA AGA GTG CTA GGG AT 3’

PCR cycling conditions:

94 - 5 minutes	1 cycle
94 - 1 minute	35 cycles
50 - 1 minute	
72 - 2 minutes	
72 - 5 minutes	1 cycle

Supplemental Table 2. Primer sequences for 3' specific *in situ* hybridization probes:

*LsAP3*for: 5´ CGATATGGGCTATGTGATAGAC 3´

*LsAP3*rev: 5´ TCAAAGGATGGAAGCTAGG 3´

*LsPI*for: 5´ CCACTCTGACCAGTATAGACAAG 3´

*LsPI*rev: 5´ GCCAAGCTATTTAGGTGACAC 3´

*LsSTK*for: 5´AGCAGCGAGCATAGTNAGCCCAG 3´

*LsSTK*rev: 5´ AAGGTGATGGAAACCTATGCAGG 3´

*LsAG*for: 5´ GTGCGGAGTTNGACACACTTCC 3

*LsAG*rev: 5´ AGCAATGACATGAGTACCC 3´

Supplemental Table 3. Primers sequences used for amplified *LsPI* and *LsAP3* full-length cDNAs. Bold letters conferred *XhoI* and *BamHI* restriction sites to the 5' and 3' ends, respectively, to allow directional cloning.

LsAP3:

*LsAP3*bam3: 5' **GGATCC**CTAGGCAAGACGAAGGTCATGGAAG 3'
*LsAP3*xho5: 5' **CTCGAG**ATGGGCAGGGGAAAGATCGAGATCAAG 3'

LsPI:

02LPIbam: 5' **GGATCC**CTATTTATTCTCTTGCAAATTTGGCTGG 3'
*LsPI*xho5: 5' **CTCGAG**ATGGGAAGGGGGAAGATCGAGATAA 3'

Supplemental Table 4. Specific primers for *LsAP3* and *LsPI* RT-PCR and Northern blot probes.

RT-PCR

LsAP3:

*LsAP3*specificF: 5' CCACACAGACAGATACCTAC 3'
*LsAP3*specificR: 5' TGAACATGTGGGGGCTCCC 3'

LsPI:

*LsPI*specificF: 5' GATCTTAACTCGCTAGGAGC 3'
*LsPI*specificR: 5' TGGGAAGCGTAATTGCGGTC 3'

Northern blot

LsAP3:

07LAP3: 5' CACCGATCTCAAGACCATCT 3'
08LAP3: 5' CACAGATGTCGTCGTCTATC 3'

LsPI:

*LsPI*specificF: 5' GATCTTAACTCGCTAGGAGC 3'
*LsPI*specificR: 5' TGGGAAGCGTAATTGCGGTC 3'

Supplemental Table 5. Phenotypic frequencies of F2 segregating population of a cross between ectopic expression line of *L. schismatica* B genes and an endogenous B gene mutant in *A. thaliana.*

35S:LsPI X *pi-1/pi-1* **EF- 303 / ABA 64-4(X)**		
Phenotype	**Observed Frequency**	**Expected Frequency**
Se/Pe, Pe, St, Ca	15	15.75
WT	4	5.25
Se/Pe, Pe, St/Ca, Ca	6	5.25
Se, Se, Ca, Ca	3	1.75
$X^2_{0.95} = 1.3324,$ (N = 28).		
35S:LsAP3 X *ap3-3/ap3-3* **EF-304, 305 & 306/ ABA 101-1(X), ABA 101-3(X) & ABA 102-3 (X)**		
WT	56	55.5
Se, Se, St/Ca, Ca	14	13.875
Se, Se, Ca, Ca	4	4.625
$X^2_{0.95} = 0.09008,$ (N = 74).		